

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/526,430
Source: PCR/10
Date Processed by STIC: 3/11/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

1

SERIAL NUMBER: 10/526,430

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- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ✓ **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING

DATE: 03/11/2005

PATENT APPLICATION: US/10/526,430

TIME: 08:27:19

Input Set : E:\DEBE052.txt

Output Set: N:\CRF4\03112005\J526430.raw

3 <110> APPLICANT: HECKER, MARKUS
 4 WAGNER, ANDREAS H.
 6 <120> TITLE OF INVENTION: Formulation for funneling nucleic acids into eukaryotic cells
 8 <130> FILE REFERENCE: DEBE:052US
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/526,430
 11 <141> CURRENT FILING DATE: 2005-03-01
 13 <150> PRIOR APPLICATION NUMBER: PCT/DE 03/02901
 14 <151> PRIOR FILING DATE: 2003-09-02
 16 <150> PRIOR APPLICATION NUMBER: 102 40 418.6
 17 <151> PRIOR FILING DATE: 2002-09-02
 19 <160> NUMBER OF SEQ ID NOS: 15
 21 <170> SOFTWARE: Patent version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 21
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Synthetic sequence
 28 <220> FEATURE:
 W--> 29 <221> NAME/KEY: Decoy oligonucleotide
 30 <222> LOCATION: (1)..(21)
 31 <223> OTHER INFORMATION:
 W--> 33 <400> 1
 34 cgcttgatga ctcagccgga a 21
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 20
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Synthetic sequence
 41 <220> FEATURE:
 W--> 42 <221> NAME/KEY: Decoy oligonucleotide
 45 <222> LOCATION: (1)..(20)
 46 <223> OTHER INFORMATION:
 W--> 48 <400> 2
 49 tgcagattgc gcaatctgca 20
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 25
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Synthetic sequence
 56 <220> FEATURE:
 W--> 57 <221> NAME/KEY: Decoy oligonucleotide
 58 <222> LOCATION: (1)..(25)
 59 <223> OTHER INFORMATION:
 W--> 61 <400> 3
 62 catgttatgc atattcctgt aagtg 25
 64 <210> SEQ ID NO: 4

pp 1-4

Does Not Comply
Corrected Diskette Needed
(see item 10 on Euro Summary Sheet)Explanation for Artificial Sequence goes
on <223> line. See 1.823
of Sequence Rules.

RAW SEQUENCE LISTING

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DATE: 03/11/2005

TIME: 08:27:19

Input Set : E:\DEBE052.txt

Output Set: N:\CRF4\03112005\J526430.raw

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65 <211> LENGTH: 17
66 <212> TYPE: DNA
67 <213> ORGANISM: Synthetic sequence
69 <220> FEATURE:
W--> 70 <221> NAME/KEY: Antisense oligonucleotide
71 <222> LOCATION: (1)..(17)
72 <223> OTHER INFORMATION:
W--> 74 <400> 4
75 atgtccctcc gagtcta 17
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 17
79 <212> TYPE: DNA
80 <213> ORGANISM: Synthetic sequence
82 <220> FEATURE:
W--> 83 <221> NAME/KEY: Antisense oligonucleotide
87 <222> LOCATION: (1)..(17)
88 <223> OTHER INFORMATION:
W--> 90 <400> 5
91 ctcgatacctg actactg 17
93 <210> SEQ ID NO: 6
94 <211> LENGTH: 17
95 <212> TYPE: DNA
96 <213> ORGANISM: Synthetic sequence
98 <220> FEATURE:
W--> 99 <221> NAME/KEY: Antisense oligonucleotide
100 <222> LOCATION: (1)..(17)
101 <223> OTHER INFORMATION:
W--> 103 <400> 6
104 caaaggtagc acacgag 17
106 <210> SEQ ID NO: 7
107 <211> LENGTH: 17
108 <212> TYPE: DNA
109 <213> ORGANISM: Synthetic sequence
111 <220> FEATURE:
W--> 112 <221> NAME/KEY: Antisense oligonucleotide
113 <222> LOCATION: (1)..(17)
114 <223> OTHER INFORMATION:
W--> 116 <400> 7
117 acatggacac gaagcag 17
119 <210> SEQ ID NO: 8
120 <211> LENGTH: 25
121 <212> TYPE: DNA
122 <213> ORGANISM: Synthetic sequence
124 <220> FEATURE:
W--> 125 <221> NAME/KEY: Primer
128 <222> LOCATION: (1)..(25)
129 <223> OTHER INFORMATION:
W--> 130 <400> 8
131 caaggtcagc aactacagcc gaggg 25

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/526,430

DATE: 03/11/2005

TIME: 08:27:19

Input Set : E:\DEBE052.txt

Output Set: N:\CRF4\03112005\J526430.raw

133 <210> SEQ ID NO: 9
134 <211> LENGTH: 24
135 <212> TYPE: DNA
136 <213> ORGANISM: Synthetic sequence
138 <220> FEATURE:
W--> 139 <221> NAME/KEY: Primer
140 <222> LOCATION: (1)..(24)
141 <223> OTHER INFORMATION:
W--> 143 <400> 9
144 tgagcagcca cagcagcatt aggg 24
146 <210> SEQ ID NO: 10
147 <211> LENGTH: 24
148 <212> TYPE: DNA
149 <213> ORGANISM: Synthetic sequence
151 <220> FEATURE:
W--> 152 <221> NAME/KEY: Primer
153 <222> LOCATION: (1)..(24)
154 <223> OTHER INFORMATION:
W--> 156 <400> 10
157 ctgtgtagcc accatgtgca gtgc 24
159 <210> SEQ ID NO: 11
160 <211> LENGTH: 22
161 <212> TYPE: DNA
162 <213> ORGANISM: Synthetic sequence
164 <220> FEATURE:
W--> 165 <221> NAME/KEY: Primer
169 <222> LOCATION: (1)..(22)
170 <223> OTHER INFORMATION:
W--> 172 <400> 11
173 tgtgacaatc ctcccaccag cg 22
175 <210> SEQ ID NO: 12
176 <211> LENGTH: 24
177 <212> TYPE: DNA
178 <213> ORGANISM: Synthetic sequence
180 <220> FEATURE:
W--> 181 <221> NAME/KEY: Primer
182 <222> LOCATION: (1)..(24)
183 <223> OTHER INFORMATION:
W--> 185 <400> 12
186 ccaagcgcag cctctttcttc aacc 24
188 <210> SEQ ID NO: 13
189 <211> LENGTH: 26
190 <212> TYPE: DNA
191 <213> ORGANISM: Synthetic sequence
193 <220> FEATURE:
W--> 194 <221> NAME/KEY: Primer
195 <222> LOCATION: (1)..(26)
196 <223> OTHER INFORMATION:
W--> 198 <400> 13

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/526,430

DATE: 03/11/2005

TIME: 08:27:19

Input Set : E:\DEBE052.txt

Output Set: N:\CRF4\03112005\J526430.raw

199 ccagcagcgt ggaggcagca tctgcc 26
201 <210> SEQ ID NO: 14
202 <211> LENGTH: 22
203 <212> TYPE: DNA
204 <213> ORGANISM: Synthetic sequence
206 <220> FEATURE:
W--> 207 <221> NAME/KEY: Primer
210 <222> LOCATION: (1)..(22)
211 <223> OTHER INFORMATION:
W--> 213 <400> 14
214 ccacgcgccac ctttcagatt gc 22
216 <210> SEQ ID NO: 15
217 <211> LENGTH: 25
218 <212> TYPE: DNA
219 <213> ORGANISM: Synthetic sequence
221 <220> FEATURE:
W--> 222 <221> NAME/KEY: Primer
223 <222> LOCATION: (1)..(25)
224 <223> OTHER INFORMATION:
W--> 225 <400> 15
226 cggagtataa ctggaactgc ttgcg 25

VERIFICATION SUMMARY

DATE: 03/11/2005

PATENT APPLICATION: US/10/526,430

TIME: 08:27:20

Input Set : E:\DEBE052.txt

Output Set: N:\CRF4\03112005\J526430.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:42 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:46
L:57 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:61 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:59
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:74 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:72
L:83 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:88
L:99 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:101
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:116 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:114
L:125 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:130 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:129
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:143 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:141
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:156 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:154
L:165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:172 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:170
L:181 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:185 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:183
L:194 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:198 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:196
L:207 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:213 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:211
L:222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:225 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:224